

P. Gambel

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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/425,516

DATE: 04/03/2001
TIME: 22:47:28

INPUT SET: S36589.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

ENTERED

1
2
3 (1) General Information:
4
5 (i) APPLICANT: Freeman, Gordon J.
6 Nadler, Lee M.
7 Gray, Gary S.
8
9 (ii) TITLE OF INVENTION: Novel CTLA4/CD28 Ligands and
10 Uses Therefor
11
12 (iii) NUMBER OF SEQUENCES: 55
13
14 (iv) CORRESPONDENCE ADDRESS:
15 (A) ADDRESSEE: LAHIVE & COCKFIELD, LLP
16 (B) STREET: 60 State Street
17 (C) CITY: Boston
18 (D) STATE: Massachusetts
19 (E) COUNTRY: USA
20 (F) ZIP: 02109
21
22 (v) COMPUTER READABLE FORM:
23 (A) MEDIUM TYPE: Floppy disk
24 (B) COMPUTER: IBM PC compatible
25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
26 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
27
28 (vi) CURRENT APPLICATION DATA:
29 (A) APPLICATION NUMBER: 09/425,516
30 (B) FILING DATE:
31 (C) CLASSIFICATION:
32
33 (vii) PRIOR APPLICATION DATA:
34 (A) APPLICATION NUMBER: 08/479,744
35 (B) FILING DATE: June 7, 1995
36 (A) APPLICATION NUMBER: 08/280,757
37 (B) FILING DATE: 26-JUL-1994
38 (A) APPLICATION NUMBER: 08/109,393
39 (B) FILING DATE: 28-AUG-1993
40 (A) APPLICATION NUMBER: 08/101,624
41 (B) FILING DATE: 26-JULY-1993
42 (A) APPLICATION NUMBER: 08/147,773
43 (B) FILING DATE: 3-NOV-1993
44
45 (viii) ATTORNEY/AGENT INFORMATION:
46

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47 (A) NAME: Mandragouras, Amy E.
48 (B) REGISTRATION NUMBER: 36,207
49 (C) REFERENCE/DOCKET NUMBER: RPI-004CP3
50
51 (ix) TELECOMMUNICATION INFORMATION:
52 (A) TELEPHONE: (617) 227-7400
53 (B) TELEFAX: (617) 227-5941
54
55
56 (2) INFORMATION FOR SEQ ID NO:1:
57
58
59 (i) SEQUENCE CHARACTERISTICS:
60 (A) LENGTH: 1120 base pairs
61 (B) TYPE: nucleic acid
62 (C) STRANDEDNESS: single
63 (D) TOPOLOGY: linear
64
65 (ii) MOLECULE TYPE: cDNA
66
67 (ix) FEATURE:
68 (A) NAME/KEY: CDS
69 (B) LOCATION: 107..1093
70
71
72 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
73
74 CACAGGGTGA AAGCTTTGCT TCTCTGCTGC TGTAACAGGG ACTAGCACAG ACACACGGAT 60
75
76 GAGTGGGGTC ATTTCCAGAT ATTAGGTCAC AGCAGAAGCA GCCAAA ATG GAT CCC 115
77 Met Asp Pro
78 1
79
80 CAG TGC ACT ATG GGA CTG AGT AAC ATT CTC TTT GTG ATG GCC TTC CTG 163
81 Gln Cys Thr Met Gly Leu Ser Asn Ile Leu Phe Val Met Ala Phe Leu
82 5 10 15
83
84 CTC TCT GGT GCT GCT CCT CTG AAG ATT CAA GCT TAT TTC AAT GAG ACT 211
85 Leu Ser Gly Ala Ala Pro Leu Lys Ile Gln Ala Tyr Phe Asn Glu Thr
86 20 25 30 35
87
88 GCA GAC CTG CCA TGC CAA TTT GCA AAC TCT CAA AAC CAA AGC CTG AGT 259
89 Ala Asp Leu Pro Cys Gln Phe Ala Asn Ser Gln Asn Gln Ser Leu Ser
90 40 45 50
91
92 GAG CTA GTA GTA TTT TGG CAG GAC CAG GAA AAC TTG GTT CTG AAT GAG 307
93 Glu Leu Val Val Phe Trp Gln Asp Gln Glu Asn Leu Val Leu Asn Glu
94 55 60 65
95
96 GTA TAC TTA GGC AAA GAG AAA TTT GAC AGT GTT CAT TCC AAG TAT ATG 355
97 Val Tyr Leu Gly Lys Glu Lys Phe Asp Ser Val His Ser Lys Tyr Met
98 70 75 80
99

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100	GGC CGC ACA AGT TTT GAT TCG GAC AGT TGG ACC CTG AGA CTT CAC AAT	403
101	Gly Arg Thr Ser Phe Asp Ser Asp Ser Trp Thr Leu Arg Leu His Asn	
102	85 90 95	
103		
104	CTT CAG ATC AAG GAC AAG GGC TTG TAT CAA TGT ATC ATC CAT CAC AAA	451
105	Leu Gln Ile Lys Asp Lys Gly Leu Tyr Gln Cys Ile Ile His His Lys	
106	100 105 110 115	
107		
108	AAG CCC ACA GGA ATG ATT CGC ATC CAC CAG ATG AAT TCT GAA CTG TCA	499
109	Lys Pro Thr Gly Met Ile Arg Ile His Gln Met Asn Ser Glu Leu Ser	
110	120 125 130	
111		
112	GTG CTT GCT AAC TTC AGT CAA CCT GAA ATA GTA CCA ATT TCT AAT ATA	547
113	Val Leu Ala Asn Phe Ser Gln Pro Glu Ile Val Pro Ile Ser Asn Ile	
114	135 140 145	
115		
116		
117	ACA GAA AAT GTG TAC ATA AAT TTG ACC TGC TCA TCT ATA CAC GGT TAC	595
118	Thr Glu Asn Val Tyr Ile Asn Leu Thr Cys Ser Ser Ile His Gly Tyr	
119	150 155 160	
120		
121	CCA GAA CCT AAG AAG ATG AGT GTT TTG CTA AGA ACC AAG AAT TCA ACT	643
122	Pro Glu Pro Lys Lys Met Ser Val Leu Leu Arg Thr Lys Asn Ser Thr	
123	165 170 175	
124		
125	ATC GAG TAT GAT GGT ATT ATG CAG AAA TCT CAA GAT AAT GTC ACA GAA	691
126	Ile Glu Tyr Asp Gly Ile Met Gln Lys Ser Gln Asp Asn Val Thr Glu	
127	180 185 190 195	
128		
129	CTG TAC GAC GTT TCC ATC AGC TTG TCT GTT TCA TTC CCT GAT GTT ACG	739
130	Leu Tyr Asp Val Ser Ile Ser Leu Ser Val Ser Phe Pro Asp Val Thr	
131	200 205 210	
132		
133	AGC AAT ATG ACC ATC TTC TGT ATT CTG GAA ACT GAC AAG ACG CGG CTT	787
134	Ser Asn Met Thr Ile Phe Cys Ile Leu Glu Thr Asp Lys Thr Arg Leu	
135	215 220 225	
136		
137	TTA TCT TCA CCT TTC TCT ATA GAG CTT GAG GAC CCT CAG CCT CCC CCA	835
138	Leu Ser Ser Pro Phe Ser Ile Glu Leu Glu Asp Pro Gln Pro Pro Pro	
139	230 235 240	
140		
141	GAC CAC ATT CCT TGG ATT ACA GCT GTA CTT CCA ACA GTT ATT ATA TGT	883
142	Asp His Ile Pro Trp Ile Thr Ala Val Leu Pro Thr Val Ile Ile Cys	
143	245 250 255	
144		
145	GTG ATG GTT TTC TGT CTA ATT CTA TGG AAA TGG AAG AAG AAG AAG CGG	931
146	Val Met Val Phe Cys Leu Ile Leu Trp Lys Trp Lys Lys Lys Lys Arg	
147	260 265 270 275	
148		
149	CCT CGC AAC TCT TAT AAA TGT GGA ACC AAC ACA ATG GAG AGG GAA GAG	979
150	Pro Arg Asn Ser Tyr Lys Cys Gly Thr Asn Thr Met Glu Arg Glu Glu	
151	280 285 290	
152		

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153 AGT GAA CAG ACC AAG AAA AGA GAA AAA ATC CAT ATA CCT GAA AGA TCT 1027
154 Ser Glu Gln Thr Lys Lys Arg Glu Lys Ile His Ile Pro Glu Arg Ser
155 295 300 305

156
157 GAT GAA GCC CAG CGT GTT TTT AAA AGT TCG AAG ACA TCT TCA TGC GAC 1075
158 Asp Glu Ala Gln Arg Val Phe Lys Ser Ser Lys Thr Ser Ser Cys Asp
159 310 315 320

160
161 AAA AGT GAT ACA TGT TTT TAATTAAAGA GTAAAGCCCA AAAAAAA 1120
162 Lys Ser Asp Thr Cys Phe
163 325

164

165

166 (2) INFORMATION FOR SEQ ID NO:2:

167

168 (i) SEQUENCE CHARACTERISTICS:

169 (A) LENGTH: 329 amino acids

170 (B) TYPE: amino acid

171 (D) TOPOLOGY: linear

172

173 (ii) MOLECULE TYPE: protein

174

175 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

176

177 Met Asp Pro Gln Cys Thr Met Gly Leu Ser Asn Ile Leu Phe Val Met
178 1 5 10 15

179

180 Ala Phe Leu Leu Ser Gly Ala Ala Pro Leu Lys Ile Gln Ala Tyr Phe
181 20 25 30

182

183 Asn Glu Thr Ala Asp Leu Pro Cys Gln Phe Ala Asn Ser Gln Asn Gln
184 35 40 45

185

186 Ser Leu Ser Glu Leu Val Val Phe Trp Gln Asp Gln Glu Asn Leu Val
187 50 55 60

188

189 Leu Asn Glu Val Tyr Leu Gly Lys Glu Lys Phe Asp Ser Val His Ser
190 65 70 75 80

191

192 Lys Tyr Met Gly Arg Thr Ser Phe Asp Ser Asp Ser Trp Thr Leu Arg
193 85 90 95

194

195 Leu His Asn Leu Gln Ile Lys Asp Lys Gly Leu Tyr Gln Cys Ile Ile
196 100 105 110

197

198 His His Lys Lys Pro Thr Gly Met Ile Arg Ile His Gln Met Asn Ser
199 115 120 125

200

201 Glu Leu Ser Val Leu Ala Asn Phe Ser Gln Pro Glu Ile Val Pro Ile
202 130 135 140

203

204 Ser Asn Ile Thr Glu Asn Val Tyr Ile Asn Leu Thr Cys Ser Ser Ile
205 145 150 155 160

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206
207 His Gly Tyr Pro Glu Pro Lys Lys Met Ser Val Leu Leu Arg Thr Lys
208                      165                      170                      175
209
210 Asn Ser Thr Ile Glu Tyr Asp Gly Ile Met Gln Lys Ser Gln Asp Asn
211                      180                      185                      190
212
213 Val Thr Glu Leu Tyr Asp Val Ser Ile Ser Leu Ser Val Ser Phe Pro
214                      195                      200                      205
215
216 Asp Val Thr Ser Asn Met Thr Ile Phe Cys Ile Leu Glu Thr Asp Lys
217                      210                      215                      220
218
219 Thr Arg Leu Leu Ser Ser Pro Phe Ser Ile Glu Leu Glu Asp Pro Gln
220                      225                      230                      235                      240
221
222 Pro Pro Pro Asp His Ile Pro Trp Ile Thr Ala Val Leu Pro Thr Val
223                      245                      250                      255
224
225 Ile Ile Cys Val Met Val Phe Cys Leu Ile Leu Trp Lys Trp Lys Lys
226                      260                      265                      270
227
228 Lys Lys Arg Pro Arg Asn Ser Tyr Lys Cys Gly Thr Asn Thr Met Glu
229                      275                      280                      285
230
231 Arg Glu Glu Ser Glu Gln Thr Lys Lys Arg Glu Lys Ile His Ile Pro
232                      290                      295                      300
233
234 Glu Arg Ser Asp Glu Ala Gln Arg Val Phe Lys Ser Ser Lys Thr Ser
235                      305                      310                      315                      320
236
237 Ser Cys Asp Lys Ser Asp Thr Cys Phe
238                      325
239

```

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TAATACGACT CACTATAGGG

20

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs

PAGE: 1

SEQUENCE VERIFICATION REPORT
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DATE: 04/03/2001
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Line

Error

Original Text

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SEQUENCE MISSING ITEM REPORT
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< < THERE ARE NO ITEMS MISSING > >

SEQUENCE CORRECTION REPORT
PATENT APPLICATION US/09/425,516DATE: 04/03/2001
TIME: 22:47:30**INPUT SET: S36589.raw**

Line	Original Text	Corrected Text
978	(3) INFORMATION FOR SEQ ID NO:29:	(2) INFORMATION FOR SEQ ID NO:29:
1118	(H) RELEVANT RESIDUES IN SEQUENCE ID NO:29: F	(H) RELEVANT RESIDUES IN SEQ ID NO:29: From -
1182	(4) INFORMATION FOR SEQ ID NO:30:	(2) INFORMATION FOR SEQ ID NO:30:
1191	(ii) MOLECULAR TYPE: cDNA to mRNA	(ii) MOLECULE TYPE: cDNA to mRNA
1335	(5) INFORMATION FOR SEQ ID NO:31:	(2) INFORMATION FOR SEQ ID NO:31:
1418	(H) RELEVANT RESIDUES IN SEQUENCE ID NO:31: F	(H) RELEVANT RESIDUES IN SEQ ID NO:31: From -